

SEQUENCE LISTING

<110> Bartel, Paul L.  
Tavtigian, Sean V.  
Myriad Genetics, Inc.

<120> MMSC1 - An MMAC1 Interacting Protein

<130> MMSC1 Gene

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<150> US 60/071,861  
<151> 1998-01-20

<160> 65

<170> PatentIn Ver. 2.0

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3 may be any amino acid; Xaa at residue 4 may be  
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1875 1880

atgtttgttgt ttagaatatt cacaggcaga tgaagttctg agtgggtat 5836

<210> 3  
<211> 1881  
<212> PRT  
<213> Homo sapiens

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Asp Arg Leu Lys Met Lys Leu Gln Glu Lys Gly Asp Thr Ser Gln Asn  
20 25 30

Glu Lys Leu Ser Met Phe Tyr Glu Thr Leu Lys Ser Pro Leu Phe Asn  
35 40 45

Gln Ile Leu Thr Leu Gln Gln Ser Ile Lys Gln Leu Lys Gly Gln Leu  
50 55 60

Asn His Ile Pro Ser Asp Cys Ser Ala Asn Phe Asp Phe Ser Arg Lys  
65 70 75 80

Gly Leu Leu Val Phe Thr Asp Gly Ser Ile Thr Asn Gly Asn Val His  
85 90 95

Arg Pro Ser Asn Asn Ser Thr Val Ser Gly Leu Phe Pro Trp Thr Pro  
100 105 110

Lys Leu Gly Asn Glu Asp Phe Asn Ser Val Ile Gln Gln Met Ala Gln  
115 120 125

Gly Arg Gln Ile Glu Tyr Ile Asp Ile Glu Arg Pro Ser Thr Gly Gly  
130 135 140

Leu Gly Phe Ser Val Val Ala Leu Arg Ser Gln Asn Leu Gly Lys Val  
145 150 155 160

Asp Ile Phe Val Lys Asp Val Gln Pro Gly Ser Val Ala Asp Arg Asp  
165 170 175

Gln Arg Leu Lys Glu Asn Asp Gln Ile Leu Ala Ile Asn His Thr Pro  
180 185 190

Leu Asp Gln Asn Ile Ser His Gln Gln Ala Ile Ala Leu Leu Gln Gln  
195 200 205

Thr	Thr	Gly	Ser	Leu	Arg	Leu	Ile	Val	Ala	Arg	Glu	Pro	Val	His	Thr	210	215	220
Lys	Ser	Ser	Thr	Ser	Ser	Ser	Leu	Asn	Asp	Thr	Thr	Leu	Pro	Glu	Thr	225	230	235
Val	Cys	Trp	Gly	His	Val	Glu	Glu	Val	Glu	Leu	Ile	Asn	Asp	Gly	Ser	245	250	255
Gly	Leu	Gly	Phe	Gly	Ile	Val	Gly	Gly	Lys	Thr	Ser	Gly	Val	Val	Val	260	265	270
Arg	Thr	Ile	Val	Pro	Gly	Gly	Leu	Ala	Asp	Arg	Asp	Gly	Arg	Leu	Gln	275	280	285
Thr	Gly	Asp	His	Ile	Leu	Lys	Ile	Gly	Gly	Thr	Asn	Val	Gln	Gly	Met	290	295	300
Thr	Ser	Glu	Gln	Val	Ala	Gln	Val	Leu	Arg	Asn	Cys	Gly	Asn	Ser	Val	305	310	315
Arg	Met	Leu	Val	Ala	Arg	Asp	Pro	Ala	Gly	Asp	Ile	Ser	Val	Thr	Pro	325	330	335
Pro	Ala	Pro	Ala	Ala	Leu	Pro	Val	Ala	Leu	Pro	Thr	Val	Ala	Ser	Lys	340	345	350
Gly	Pro	Gly	Ser	Asp	Ser	Ser	Leu	Phe	Glu	Thr	Tyr	Asn	Val	Glu	Leu	355	360	365
Val	Arg	Lys	Asp	Gly	Gln	Ser	Leu	Gly	Ile	Arg	Ile	Val	Gly	Tyr	Val	370	375	380
Gly	Thr	Ser	His	Thr	Gly	Glu	Ala	Ser	Gly	Ile	Tyr	Val	Lys	Ser	Val	385	390	395
Ile	Pro	Gly	Ser	Ala	Ala	Tyr	His	Asn	Gly	His	Ile	Gln	Val	Asn	Asp	405	410	415
Lys	Ile	Val	Ala	Val	Asp	Gly	Val	Asn	Ile	Gln	Gly	Phe	Ala	Asn	His	420	425	430
Asp	Val	Val	Glu	Val	Leu	Arg	Asn	Ala	Gly	Gln	Val	Val	His	Leu	Thr	435	440	445
Leu	Val	Arg	Arg	Lys	Thr	Ser	Ser	Ser	Thr	Ser	Pro	Leu	Glu	Pro	Pro	450	455	460
Ser	Asp	Arg	Gly	Thr	Val	Val	Glu	Pro	Leu	Lys	Pro	Pro	Ala	Leu	Phe	465	470	475
Leu	Thr	Gly	Ala	Val	Glu	Thr	Glu	Thr	Asn	Val	Asp	Gly	Glu	Asp	Glu	485	490	495
Glu	Ile	Lys	Glu	Arg	Ile	Asp	Thr	Leu	Lys	Asn	Asp	Asn	Ile	Gln	Ala	500	505	510
Leu	Glu	Lys	Leu	Glu	Lys	Val	Pro	Asp	Ser	Pro	Glu	Asn	Glu	Leu	Lys	515	520	525
Ser	Arg	Trp	Glu	Asn	Leu	Leu	Gly	Pro	Asp	Tyr	Glu	Val	Met	Val	Ala	530	535	540

Thr	Leu	Asp	Thr	Gln	Ile	Ala	Asp	Asp	Ala	Glu	Leu	Gln	Lys	Tyr	Ser	545	550	555	560
Lys	Leu	Leu	Pro	Ile	His	Thr	Leu	Arg	Leu	Gly	Val	Glu	Val	Asp	Ser	565	570	575	
Phe	Asp	Gly	His	His	Tyr	Ile	Ser	Ser	Ile	Val	Ser	Gly	Gly	Pro	Val	580	585	590	
Asp	Thr	Leu	Gly	Leu	Leu	Gln	Pro	Glu	Asp	Glu	Leu	Leu	Glu	Val	Asn	595	600	605	
Gly	Met	Gln	Leu	Tyr	Gly	Lys	Ser	Arg	Arg	Glu	Ala	Val	Ser	Phe	Leu	610	615	620	
Lys	Glu	Val	Pro	Pro	Pro	Phe	Thr	Leu	Val	Cys	Cys	Arg	Arg	Leu	Phe	625	630	635	640
Asp	Asp	Glu	Ala	Ser	Val	Asp	Glu	Pro	Arg	Arg	Thr	Glu	Thr	Ser	Leu	645	650	655	
Pro	Glu	Thr	Glu	Val	Asp	His	Asn	Met	Asp	Val	Asn	Thr	Glu	Glu	Asp	660	665	670	
Asp	Asp	Gly	Glu	Leu	Ala	Leu	Trp	Ser	Pro	Glu	Val	Lys	Ile	Val	Glu	675	680	685	
Leu	Val	Lys	Asp	Cys	Lys	Gly	Leu	Gly	Phe	Ser	Ile	Leu	Asp	Tyr	Gln	690	695	700	
Asp	Pro	Leu	Asp	Pro	Thr	Arg	Ser	Val	Ile	Val	Ile	Arg	Ser	Leu	Val	705	710	715	720
Ala	Asp	Gly	Val	Ala	Glu	Arg	Ser	Gly	Gly	Leu	Leu	Pro	Gly	Asp	Arg	725	730	735	
Leu	Val	Ser	Val	Asn	Glu	Tyr	Cys	Leu	Asp	Asn	Thr	Ser	Leu	Ala	Glu	740	745	750	
Ala	Val	Glu	Ile	Leu	Lys	Ala	Val	Pro	Pro	Gly	Leu	Val	His	Leu	Gly	755	760	765	
Ile	Cys	Lys	Pro	Leu	Val	Glu	Asp	Asn	Glu	Glu	Glu	Ser	Cys	Tyr	Ile	770	775	780	
Leu	His	Ser	Ser	Ser	Asn	Glu	Asp	Lys	Thr	Glu	Phe	Ser	Gly	Thr	Ile	785	790	795	800
His	Asp	Ile	Asn	Ser	Ser	Leu	Ile	Leu	Glu	Ala	Pro	Lys	Gly	Phe	Arg	805	810	815	
Asp	Glu	Pro	Tyr	Phe	Lys	Glu	Glu	Leu	Val	Asp	Glu	Pro	Phe	Leu	Asp	820	825	830	
Leu	Gly	Lys	Ser	Phe	His	Ser	Gln	Gln	Lys	Glu	Ile	Glu	Gln	Ser	Lys	835	840	845	
Glu	Ala	Trp	Glu	Met	His	Glu	Phe	Leu	Thr	Pro	Arg	Leu	Gln	Glu	Met	850	855	860	
Asp	Glu	Glu	Arg	Glu	Met	Leu	Val	Asp	Glu	Glu	Tyr	Glu	Leu	Tyr	Gln	865	870	875	880

Asp Pro Ser Pro Ser Met Glu Leu Tyr Pro Leu Ser His Ile Gln Glu  
885 890 895

Ala Thr Pro Val Pro Ser Val Asn Glu Leu His Phe Gly Thr Gln Trp  
900 905 910

Leu His Asp Asn Glu Pro Ser Glu Ser Gln Glu Ala Arg Thr Gly Arg  
915 920 925

Thr Val Tyr Ser Gln Glu Ala Gln Pro Tyr Gly Tyr Cys Pro Glu Asn  
930 935 940

Val Met Lys Glu Asn Phe Val Met Glu Ser Leu Pro Ser Val Pro Ser  
945 950 955 960

Thr Glu Gly Asn Ser Gln Gln Gly Arg Phe Asp Asp Leu Glu Asn Leu  
965 970 975

Asn Ser Leu Ala Lys Thr Ser Leu Asp Leu Gly Met Ile Pro Asn Asp  
980 985 990

Val Gln Gly Pro Ser Leu Leu Ile Asp Leu Pro Val Val Ala Gln Arg  
995 1000 1005

Arg Glu Gln Glu Asp Leu Pro Leu Tyr Gln His Gln Ala Thr Arg Val  
1010 1015 1020

Ile Ser Lys Ala Ser Ala Tyr Thr Gly Met Leu Ser Ser Arg Tyr Ala  
1025 1030 1035 1040

Thr Asp Thr Cys Glu Leu Pro Glu Arg Glu Glu Gly Glu Gly Glu Glu  
1045 1050 1055

Thr Pro Asn Phe Ser His Trp Gly Pro Pro Arg Ile Val Glu Ile Phe  
1060 1065 1070

Arg Glu Pro Asn Val Ser Leu Gly Ile Ser Ile Val Gly Gly Gln Thr  
1075 1080 1085

Val Ile Lys Arg Leu Lys Asn Gly Glu Glu Leu Lys Gly Ile Phe Ile  
1090 1095 1100

Lys Gln Val Leu Glu Asp Ser Pro Ala Gly Lys Thr Asn Ala Leu Lys  
1105 1110 1115 1120

Thr Gly Asp Lys Ile Leu Glu Val Ser Gly Val Asp Leu Gln Asn Ala  
1125 1130 1135

Ser His Ser Glu Ala Val Glu Ala Ile Lys Asn Ala Gly Asn Pro Val  
1140 1145 1150

Val Phe Ile Val Gln Ser Leu Ser Ser Thr Pro Arg Val Ile Pro Asn  
1155 1160 1165

Val His Asn Lys Ala Asn Lys Ile Thr Ser Asn Gln Asn Gln Asp Thr  
1170 1175 1180

Gln Glu Lys Lys Glu Lys Arg Gln Gly Thr Ala Pro Pro Pro Met Lys  
1185 1190 1195 1200

Leu Pro Pro Pro Tyr Lys Ala Leu Thr Asp Asp Ser Asp Glu Asn Glu  
1205 1210 1215

Glu Glu Asp Ala Phe Thr Asp Gln Lys Ile Arg Gln Arg Tyr Ala Asp  
 1220 1225 1230  
 Leu Pro Gly Glu Leu His Ile Ile Glu Leu Glu Lys Asp Lys Asn Gly  
 1235 1240 1245  
 Leu Gly Leu Ser Leu Ala Gly Asn Lys Asp Arg Ser Arg Met Ser Ile  
 1250 1255 1260  
 Phe Val Val Gly Ile Asn Pro Glu Gly Pro Ala Ala Ala Asp Gly Arg  
 265 1270 1275 1280  
 Met His Ile Gly Asp Glu Leu Leu Glu Ile Asn Asn Gln Ile Leu Tyr  
 1285 1290 1295  
 Gly Arg Ser His Gln Asn Ala Ser Ala Ile Ile Lys Thr Ala Pro Ser  
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 Lys Val Lys Leu Val Phe Ile Arg Asn Glu Asp Ala Val Asn Gln Met  
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 Ala Val Thr Pro Phe Pro Val Pro Ser Ser Ser Pro Ser Ser Ile Glu  
 1330 1335 1340  
 Asp Gln Ser Gly Thr Glu Pro Ile Ser Ser Glu Glu Asp Gly Ser Leu  
 345 1350 1355 1360  
 Glu Val Gly Ile Lys Gln Leu Pro Glu Ser Glu Ser Phe Lys Leu Ala  
 1365 1370 1375  
 Val Ser Gln Met Lys Gln Gln Lys Tyr Pro Thr Lys Val Ser Phe Ser  
 1380 1385 1390  
 Ser Gln Glu Ile Pro Leu Ala Pro Ala Ser Ser Tyr His Ser Thr Asp  
 1395 1400 1405  
 Ala Asp Phe Thr Gly Tyr Gly Gly Phe Gln Ala Pro Leu Ser Val Asp  
 1410 1415 1420  
 Pro Ala Thr Cys Pro Ile Val Pro Gly Gln Glu Met Ile Ile Glu Ile  
 425 1430 1435 1440  
 Ser Lys Gly Arg Ser Gly Leu Gly Leu Ser Ile Val Gly Gly Lys Asp  
 1445 1450 1455  
 Thr Pro Leu Asn Ala Ile Val Ile His Glu Val Tyr Glu Glu Gly Ala  
 1460 1465 1470  
 Ala Ala Arg Asp Gly Arg Leu Trp Ala Gly Asp Gln Ile Leu Glu Val  
 1475 1480 1485  
 Asn Gly Val Asp Leu Arg Asn Ser Ser His Glu Glu Ala Ile Thr Ala  
 1490 1495 1500  
 Leu Arg Gln Thr Pro Gln Lys Val Arg Leu Val Val Tyr Arg Asp Glu  
 505 1510 1515 1520  
 Ala His Tyr Arg Asp Glu Glu Asn Leu Glu Ile Phe Pro Val Asp Leu  
 1525 1530 1535  
 Gln Lys Lys Ala Gly Arg Gly Leu Gly Leu Ser Ile Val Gly Lys Arg  
 1540 1545 1550

Asn Gly Ser Gly Val Phe Ile Ser Asp Ile Val Lys Gly Gly Ala Ala  
 1555 1560 1565  
 Asp Leu Asp Gly Arg Leu Ile Gln Gly Asp Gln Ile Leu Ser Val Asn  
 1570 1575 1580  
 Gly Glu Asp Met Arg Asn Ala Ser Gln Glu Thr Val Ala Thr Ile Leu  
 585 1590 1595 1600  
 Lys Cys Ala Gln Gly Leu Val Gln Leu Glu Ile Gly Arg Leu Arg Ala  
 1605 1610 1615  
 Gly Ser Trp Thr Ser Ala Arg Thr Thr Ser Gln Asn Ser Gln Gly Ser  
 1620 1625 1630  
 Gln Gln Ser Ala His Ser Ser Cys His Pro Ser Phe Ala Pro Val Ile  
 1635 1640 1645  
 Thr Gly Leu Gln Asn Leu Val Gly Thr Lys Arg Val Ser Asp Pro Ser  
 1650 1655 1660  
 Gln Lys Asn Ser Gly Thr Asp Met Glu Pro Arg Thr Val Glu Ile Asn  
 665 1670 1675 1680  
 Arg Glu Leu Ser Asp Ala Leu Gly Ile Ser Ile Ala Gly Gly Arg Gly  
 1685 1690 1695  
 Ser Pro Leu Gly Asp Ile Pro Val Phe Ile Ala Met Ile Gln Ala Ser  
 1700 1705 1710  
 Gly Val Ala Ala Arg Thr Gln Lys Leu Lys Val Gly Asp Arg Ile Val  
 1715 1720 1725  
 Ser Ile Asn Gly Gln Pro Leu Asp Gly Leu Ser His Ala Asp Val Val  
 1730 1735 1740  
 Asn Leu Leu Lys Asn Ala Tyr Gly Arg Ile Ile Leu Gln Val Val Ala  
 745 1750 1755 1760  
 Asp Thr Asn Ile Ser Ala Ile Ala Ala Gln Leu Glu Asn Met Ser Thr  
 1765 1770 1775  
 Gly Tyr His Leu Gly Ser Pro Thr Ala Glu His His Pro Glu Asp Thr  
 1780 1785 1790  
 Glu Thr Pro Pro Pro Lys Ile Ile Thr Leu Glu Lys Gly Ser Glu Gly  
 1795 1800 1805  
 Leu Gly Phe Ser Ile Val Gly Gly Tyr Gly Ser Pro His Gly Asp Leu  
 1810 1815 1820  
 Pro Ile Tyr Val Lys Thr Val Phe Ala Lys Gly Ala Ala Ala Asp Asp  
 825 1830 1835 1840  
 Gly Arg Leu Lys Arg Gly Asp Gln Ile Leu Ala Val Asn Gly Glu Thr  
 1845 1850 1855  
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 1860 1865 1870  
 Arg Gly Thr Val Thr Leu Thr Val Leu  
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 Met Pro Glu Asn  
 1  
 cct gct gca gag aag atg cag gtc ctg cag gtc ctg gat cgc ctt cga 164  
 Pro Ala Ala Glu Lys Met Gln Val Leu Gln Val Leu Asp Arg Leu Arg  
 5 10 15 20  
 ggg aag ctg cag gag aag gga gac acg acg cag aac gag aag ctg tct 212  
 Gly Lys Leu Gln Glu Lys Gly Asp Thr Thr Gln Asn Glu Lys Leu Ser  
 25 30 35  
 gcg ttc tac gag acg ctg aag agc cct ctc ttc aac cag atc ctt aca 260  
 Ala Phe Tyr Glu Thr Leu Lys Ser Pro Leu Phe Asn Gln Ile Leu Thr  
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 Leu Gln Gln Ser Ile Lys Gln Leu Lys Gly  
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 <213> Mus musculus

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 Asp Arg Leu Arg Gly Lys Leu Gln Glu Lys Gly Asp Thr Thr Gln Asn  
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 Glu Lys Leu Ser Ala Phe Tyr Glu Thr Leu Lys Ser Pro Leu Phe Asn  
 35 40 45  
 Gln Ile Leu Thr Leu Gln Gln Ser Ile Lys Gln Leu Lys Gly  
 50 55 60

<210> 6  
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 <212> PRT  
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<400> 6  
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<210> 7  
 <211> 16

<212> PRT  
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<223> Description of Artificial Sequence:SH3 Binding  
Protein PDZ Domain

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Ser Gly Ser Gly Ile Leu Ala Pro Pro Val Pro Pro Arg Asn Thr Arg  
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<210> 8

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:AF6 PDZ Binding  
Protein

<400> 8

Ser Gly Asp Asp Gly Asp Asp Pro Phe Leu Gln Tyr Glu Phe Tyr Val  
1 5 10 15

<210> 9

<211> 16

<212> PRT

<213> Homo sapiens

<400> 9

Glu Asn Glu Pro Phe Asp Glu Asp Gln His Thr Gln Ile Thr Lys Val  
1 5 10 15

<210> 10

<211> 20

<212> DNA

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<223> Description of Artificial Sequence:MMSC1 Primers

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20

<210> 11

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MMSC1 Primers

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22

<210> 12

<211> 38

<212> DNA

<213> Artificial Sequence



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<210> 28  
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<223> Description of Artificial Sequence:MMSC1 Primers  
  
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<210> 30  
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<400> 30  
gtggattcct ttgatgggca cc 22  
  
<210> 31  
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aggaaacagc tatgaccatc taaaggtcc tggtaatcc 39

<210> 34  
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<400> 34  
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<210> 35  
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<400> 35  
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<210> 36  
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<400> 36  
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<210> 37  
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<400> 37  
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<400> 39  
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<210> 41  
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<400> 41  
caaatatgct catgcgtgat cgg 23

<210> 42  
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<400> 44

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39

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-27-

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39